PTO/SB/17 (10-03)

FEE TRANSMITTAL for FY 2004

Effective 10/01/2003. Patent fees are subject to annual revision.

☒ Applicant claims small entity status. See 37 CFR 1.27

TOTAL AMOUNT OF PAYMENT | ($) 385

Complete If Known	
Application Number	
Filing Date	March 11, 2004
First Named Inventor	Gilbert, Michel
Examiner Name	
Art Unit	
Attorney Docket No.	019633-000912US

METHOD OF PAYMENT *(check all that apply)*

☐ Check ☐ Credit Card ☐ Money Order ☐ Other ☐ None

☒ Deposit Account:

Deposit Account Number: 20-1430

Deposit Account Name: Townsend and Townsend and Crew LLP

The Director is authorized to: *(check all that apply)*

☒ Charge fee(s) indicated below ☒ Credit any overpayments

☒ Charge any additional fee(s) or any underpayment of fee(s)

☐ Charge fee(s) indicated below, except for the filing fee to the above-identified deposit account.

FEE CALCULATION

1. BASIC FILING FEE

Large Entity Fee Code	Large Entity Fee ($)	Small Entity Fee Code	Small Entity Fee ($)	Fee Description	Fee Paid
1001	770	2001	385	Utility filing fee	385
1002	340	2002	170	Design filing fee	
1003	530	2003	265	Plant filing fee	
1004	770	2004	385	Reissue filing fee	
1005	160	2005	80	Provisional filing fee	

SUBTOTAL (1) ($)385

2. EXTRA CLAIM FEES FOR UTILITY AND REISSUE

			Extra Claims	Fee from below	Fee Paid
Total Claims	16	-20** =	0	X$9 =	$0
Independent Claims	1	-3** =	0	X$43 =	$0
Multiple Dependent				X =	

Large Entity Fee Code	Large Entity Fee ($)	Small Entity Fee Code	Small Entity Fee ($)	Fee Description
1202	18	2202	9	Claims in excess of 20
1201	86	2201	43	Independent claims in excess of 3
1203	290	2203	145	Multiple dependent claim, if not paid
1204	86	2204	43	** Reissue independent claims over original patent
1205	18	2205	9	** Reissue claims in excess of 20 and over original patent

SUBTOTAL (2) ($)0

**or number previously paid, if greater; For Reissues, see above

FEE CALCULATION (continued)

3. ADDITIONAL FEES

Large Entity Fee Code	Large Entity Fee ($)	Small Entity Fee Code	Small Entity Fee ($)	Fee Description	Fee Paid
1051	130	2051	65	Surcharge - late filing fee or oath	
1052	50	2052	25	Surcharge - late provisional filing fee or cover sheet.	
1053	130	1053	130	Non-English specification	
1812	2,520	1812	2,520	For filing a request for reexamination	
1804	920*	1804	920*	Requesting publication of SIR prior to Examiner action	
1805	1,840*	1805	1,840*	Requesting publication of SIR after Examiner action	
1251	110	2251	55	Extension for reply within first month	
1252	420	2252	210	Extension for reply within second month	
1253	950	2253	475	Extension for reply within third month	
1254	1,480	2254	740	Extension for reply within fourth month	
1255	2,010	2255	1,005	Extension for reply within fifth month	
1401	330	2401	165	Notice of Appeal	
1402	330	2402	165	Filing a brief in support of an appeal	
1403	290	2403	145	Request for oral hearing	
1451	1,510	1451	1,510	Petition to institute a public use proceeding	
1452	110	2452	55	Petition to revive – unavoidable	
1453	1,330	2453	665	Petition to revive – unintentional	
1501	1,330	2501	665	Utility issue fee (or reissue)	
1502	480	2502	240	Design issue fee	
1503	640	2503	320	Plant issue fee	
1460	130	1460	130	Petitions to the Commissioner	
1807	50	1807	50	Petitions related to provisional applications	
1806	180	1806	180	Submission of Information Disclosure Stmt	
8021	40	8021	40	Recording each patent assignment per property (times number of properties)	
1809	770	2809	385	Filing a submission after final rejection (37 CFR § 1.129(a))	
1810	770	2810	385	For each additional invention to be examined (37 CFR § 1.129(b))	
1801	770	2801	385	Request for Continued Examination (RCE)	
1802	900	1802	900	Request for expedited examination of a design application	

Other fee (specify) _____

*Reduced by Basic Filing Fee Paid SUBTOTAL (3) ($)

SUBMITTED BY				Complete *(if applicable)*	
Name (Print/Type)	Beth L. Kelly	*Registration No. (Attorney/Agent)*	51,868	*Telephone*	415-576-0200
Signature	Beth L Kelly			*Date*	March 11, 2004

WARNING: Information on this form may become public. Credit card information should not be included on this form. Provide credit card information and authorization on PTO-2038.

60163784 v1

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MAR 3 0 2007

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:	Confirmation No. 7215
GILBERT and WAKARCHUK	Examiner: Portner, Virginia Allen
Application No.: 10/799,016	Technology Center/Art Unit: 1645
Filed: March 11, 2004	TERMINAL DISCLAIMER
For: LIPOPOLYSACCHARIDE A-2,3 SIALYLTRANSFERASE OF CAMPYLOBACTER JEJUNI AND ITS USES	
Customer No.: 20350	

Mail Stop Amendment
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

Petitioner, National Research Council of Canada, Inc., is the owner of 100 percent interest in the instant application. Petitioner hereby disclaims, except as provided below, the terminal part of the statutory term of any patent granted on the instant application, which would extend beyond the expiration date of the full statutory term defined in 35 U.S.C. 154 to 156 and 173 as shortened by any terminal disclaimer filed prior to the grant of U.S. Patent No. 6,709,834 (filed January 29, 2002).

U.S. Patent No. 6,709,834 and the instant application were commonly owned at that time of invention of the subject matter claimed in U.S. Patent No. 6,709,834. Petitioner hereby agrees that any patent so granted on the instant application shall be enforceable only for and during such period that it and U.S. Patent No. 6,709,834 are commonly owned. This agreement runs with any patent granted on the instant application and is binding upon the grantee, its successors or assigns.

In making the above disclaimer, petitioner does not disclaim the terminal part of any patent granted on the instant application that would extend to the expiration date of the full

statutory term as deemed in 35 U.S.C. 154 to 156 and 173 of a patent granted from U.S. Patent No. 6,709,834, as shortened by any terminal disclaimer filed prior to the patent grant, in the event that any such patent: expires for failure to pay a maintenance fee, is held unenforceable, is found invalid by a court of competent jurisdiction, is statutorily disclaimed in whole or terminally disclaimed under 37 CFR 1.321, has all claims canceled by a reexamination certificate, is reissued, or is in any manner terminated prior to the expiration of its full statutory term as shortened by any terminal disclaimer filed prior to its grant.

For submissions on behalf of an organization (*e.g.*, corporation, partnership, university, government agency, etc.), the undersigned (whose title is supplied below) is empowered to act on behalf of the organization.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: 26 March 2007

By: Marielle Piché
Name: Marielle Piché

Title: Secretary General, EXECUTIVE OFFICES
Secretary General, Executive Offices
Secretariat

Executive Offices
National Research Council of Canada
1200 Montreal Road
M-58 Room W-312
Ottawa, ON K1A 0R6

BLK:blk
61003220 v1

Amendments to the Specification:

Please replace paragraph beginning at page 9, line 18 with the following amended paragraph:

Another example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al., J. Mol. Biol.* 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~ (ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al, supra.*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. For identifying whether a nucleic acid or polypeptide is within the scope of the invention, the default parameters of the BLAST programs are suitable. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)).

Allowance 9 Blank 3/30/07

C07K 1/00

C12Q 1/68

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-34. (cancelled)

35. (Currently amended) An isolated α-2,3-sialyltransferase polypeptide, wherein the α-2,3-sialyltransferase polypeptide catalyzes the transfer of a sialic acid from a donor substrate to an acceptor sugar,
and wherein the α-2,3-sialyltransferase polypeptide comprises ~~an~~ the amino acid sequence ~~with at least 90% identity to~~ of residues 1-328 of SEQ ID NO:2~~, over the entire length of~~ or an amino acid sequence that shares at least 95% identity with amino acid residues 1-328 of SEQ ID NO:2.

36-37. (Cancelled)

An isolated

38. (Currently amended) ~~The~~ α-2,3-sialyltransferase polypeptide ~~of claim~~ 37, wherein the α-2,3-sialyltransferase polypeptide comprises ~~an~~ the amino acid sequence ~~with at least 95% identity to~~ of residues 1-430 of SEQ ID NO:2~~, over the entire length of~~ or an amino acid sequence that shares at least 95% identity with amino acid residues 1-430 of SEQ ID NO:2.

39. (Previously presented) The α-2,3-sialyltransferase polypeptide of claim 35, wherein the α-2,3-sialyltransferase polypeptide further comprises an amino acid tag.

40. (Previously presented) The α-2,3-sialyltransferase polypeptide of claim 39, wherein the amino acid tag is a member selected from the group consisting of polyhistidine, maltose binding protein, myc, V-5, and DYKDDDK (SEQ ID NO:8).

41. (Previously presented) A method of adding a sialic acid residue to an acceptor molecule comprising a terminal galactose residue, the method comprising contacting

Renumbered claims

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-34. (cancelled)

1 ~~38.~~ (Currently amended) An isolated α-2,3-sialyltransferase polypeptide, wherein the α-2,3-sialyltransferase polypeptide catalyzes the transfer of a sialic acid from a donor substrate to an acceptor sugar,

and wherein the α-2,3-sialyltransferase polypeptide comprises ~~an~~ the amino acid sequence ~~with at least 90% identity to~~ of residues 1-328 of SEQ ID NO:2~~, over the entire length of~~ or an amino acid sequence that shares at least 95% identity with amino acid residues 1-328 of SEQ ID NO:2.

36-37. (Cancelled)

An isolated

4 ~~38.~~ (Currently amended) ~~The~~ α-2,3-sialyltransferase polypeptide~~, of claim 37,~~ wherein the α-2,3-sialyltransferase polypeptide comprises ~~an~~ the amino acid sequence ~~with at least 95% identity to~~ of residues 1-430 of SEQ ID NO:2~~, over the entire length of~~ or an amino acid sequence that shares at least 95% identity with amino acid residues 1-430 of SEQ ID NO:2.

2 ~~39.~~ (Previously presented) The α-2,3-sialyltransferase polypeptide of claim 1 ~~35~~, wherein the α-2,3-sialyltransferase polypeptide further comprises an amino acid tag.

3 ~~40.~~ (Previously presented) The α-2,3-sialyltransferase polypeptide of claim 2 ~~39~~, wherein the amino acid tag is a member selected from the group consisting of polyhistidine, maltose binding protein, myc, V-5, and DYKDDDK (SEQ ID NO:8).

5 ~~41.~~ (Previously presented) A method of adding a sialic acid residue to an acceptor molecule comprising a terminal galactose residue, the method comprising contacting

the acceptor molecule with an activated sialic acid molecule and an α-2,3-sialyltransferase polypeptide of claim 35 or claim 37, 38

42. (Previously presented) The method of claim 41, wherein the terminal galactose residue is linked through a linkage to a second residue in the acceptor molecule.

43. (Previously presented) The method of claim 42, wherein the linkage is a β1,4 linkage.

44. (Previously presented) The method of claim 43, wherein the second residue is a Glc or a GlcNAc.

45. (Previously presented) The method of claim 42, wherein the linkage is a β1,3 linkage.

46. (Previously presented) The method of claim 45, wherein the second residue is a GlcNAc or a GalNAc.

47. (Previously presented) The method of claim 41, wherein the activated sialic acid is CMP-Neu5Ac.

48. (Currently amended) The method of claim 41, wherein the α-2,3-sialyltransferase polypeptide comprises ~~an~~ the amino acid sequence ~~with at least 95% identity to~~ of residues 1-328 of SEQ ID NO:2~~, over the entire length of residues 1-328~~.

49. (Previously presented) The method of claim 41, wherein the α-2,3-sialyltransferase polypeptide further comprises an amino acid tag.

50. (Previously presented) The method of claim 49, wherein the amino acid tag is a member selected from the group consisting of polyhistidine, maltose binding protein, myc, V-5, and DYKDDDK (SEQ ID NO:8).

the acceptor molecule with an activated sialic acid molecule and an α-2,3-sialyltransferase polypeptide of claim ~~35~~ 1 or claim ~~37~~ 4.

~~42.~~ 10 (Previously presented) The method of claim ~~41~~ 5, wherein the terminal galactose residue is linked through a linkage to a second residue in the acceptor molecule.

~~43.~~ 11 (Previously presented) The method of claim ~~42~~ 10, wherein the linkage is a β1,4 linkage.

~~44.~~ 12 (Previously presented) The method of claim ~~43~~ 11, wherein the second residue is a Glc or a GlcNAc.

~~45.~~ 13 (Previously presented) The method of claim ~~42~~ 10, wherein the linkage is a β1,3 linkage.

~~46.~~ 14 (Previously presented) The method of claim ~~45~~ 13, wherein the second residue is a GlcNAc or a GalNAc.

~~47.~~ 6 (Previously presented) The method of claim ~~41~~ 5, wherein the activated sialic acid is CMP-Neu5Ac.

~~48.~~ 7 (Currently amended) The method of claim ~~41~~ 5, wherein the α-2,3-sialyltransferase polypeptide comprises ~~an~~ the amino acid sequence ~~with at least 95% identity to~~ of residues 1-328 of SEQ ID NO:2, ~~over the entire length of residues 1-328~~.

~~49.~~ 8 (Previously presented) The method of claim ~~41~~ 5, wherein the α-2,3-sialyltransferase polypeptide further comprises an amino acid tag.

~~50.~~ 9 (Previously presented) The method of claim ~~49~~ 8, wherein the amino acid tag is a member selected from the group consisting of polyhistidine, maltose binding protein, myc, V-5, and DYKDDDK (SEQ ID NO:8).

REMARKS/ARGUMENTS

With this amendment, claims 35, and 38-50 are pending. Claims 1-34, 36, and 37 are cancelled. For convenience, the Examiner's rejections are addressed in the order presented in a November 8, 2006 Office Action.

I. Status of the claims

Claim 35 is amended to recite wherein the α-2,3-sialyltransferase polypeptide comprises the amino acid sequence of residues 1-328 of SEQ ID NO:2 or an amino acid sequence that shares at least 95% identity with amino acid residues 1-328 of SEQ ID NO:2. Claim 38 was similarly amended and recites amino acid residues 1-430. Support for these amendments is found throughout the specification, for example, at page 4, lines 17-20 and page 8, lines 26-30. These amendments add no new matter.

II. Objections to the specification

The Office Action objects to the presence of hyperlinks in the specification. In order to expedite prosecution, the specification is amended to remove hyperlinks. In view of the above amendments, withdrawal of the specification and drawing objections is respectfully requested.

III. Rejections under 35 U.S.C. §112, first paragraph, written description

Claims 35-50 are rejected under 35 U.S.C. §112, first paragraph for allegedly failing to comply with the written description requirement. According to the Office Action, the specification does not provide description of polypeptides with at least 90-95% identity to SEQ ID NO:2. The Office Action alleges that those of skill would not recognize that the inventors had possession of the claimed invention at the time of filing.

The Office Action indicates that the written description rejection can be obviated by amending the claims to recite "wherein the α-2,3-sialyltransferase polypeptide comprises the amino acid sequence of residues 1-328 of SEQ ID NO:2 or an amino acid sequence that shares at

least 95% identity with amino acid residues 1-328 of SEQ ID NO:2." *See, i.e.*, Office Action at page 4. Applicants have amended claims 35 and 38 as suggested in the Office Action in order to expedite prosecution. It is Applicants' understanding that the amended claims overcome the rejections for alleged lack of written description. In view of these amendments and remarks, withdrawal of the rejection under 35 U.S.C. §112, first paragraph is respectfully requested.

IV. Rejections under 35 U.S.C. §102(b) and §102(e)

Claims 35-39 are rejected under 35 U.S.C. §102(b) as allegedly anticipated by Gilbert *et al. J. Biol. Chem.* 271:28217-28276 (1996) and under 35 U.S.C. §102(b) by Paulson *et al.* (U.S. Patent No. 6,399,336).

To anticipate a claim, the reference must teach every element of the claim. "A claim is anticipated only if each and every element as set forth in the claim is found...in a single prior art reference." *Verdegaal Bros. v. Union Oil of California*, 814 F.2d 628, 631, 2 USPQ2d 1051, 1053 (Fed. Cir. 1987). Thus, in order to anticipate, the cited reference must contain every element of the claims at issue.

Applicants respectfully traverse the rejection and submit that, as amended, the claims are not anticipated by the cited references. Moreover, the Office Action indicates that the anticipation rejections can be obviated by amending the claims to recite "wherein the α-2,3-sialyltransferase polypeptide comprises the amino acid sequence of residues 1-328 of SEQ ID NO:2 or an amino acid sequence that shares at least 95% identity with amino acid residues 1-328 of SEQ ID NO:2." *See, i.e.*, Office Action at page 5. In view of these amendments and remarks, withdrawal of the rejection under 35 U.S.C. §102 is respectfully requested.

V. Rejections for alleged obviousness-type double patenting

Claim 35-47 and 49-50 are rejected as allegedly unpatentable under the judicial doctrine of obviousness type double patenting over claims 1-15 of U.S. Patent No. 6,709,834. In order to expedite prosecution of this application, Applicants submit a terminal disclaimer of the term of a patent granted on the instant application over U.S. Patent No. 6,709,834. Applicants

note that the filing of a terminal disclaimer to obviate a rejection based on non-statutory double patenting is not an admission of the propriety of the rejection. See, MPEP §804.02. Accordingly, Applicants respectfully request withdrawal of this rejection.

Claims 35-40 are rejected for alleged obviousness-type double patenting over claims 43-46 of USSN 10/821,573, now US Patent No. 7,192,756 (the '756 patent), to be issued March 2007. Applicants respectfully traverse the rejection. The '756 patent claims CstII proteins that are encoded by a nucleic acid that is amplified from a *Campylobacter* genome using SEQ ID NOs:46 and 47 as the amplification primers. The present claims are directed to CstI proteins from *Campylobacter* bacteria. Applicants provide data that SEQ ID NOs:46 and 47 of the '756 patent will not amplify a nucleic acid from a *Campylobacter* genome that encodes the claimed proteins. Exhibit A provides alignments of the nucleic acid sequence of SEQ ID NO:1 from the present application with the nucleic acid sequence of SEQ ID NO:46 and the reverse complement of SEQ ID NO:47 from the '756 patent. SEQ ID NO:46 aligns poorly near the 5' end of SEQ ID NO:1 and substantial gaps are required for the alignment. Moreover, any amplified product would not include the initiating ATG codon. The reverse complement of SEQ ID NO:47 aligns poorly to SEQ ID NO:1, beginning at about nucleotide 742, and also requires substantial gaps to produce an alignment. Even if the sequence alignment and complementation was sufficient to allow hybridization and amplification of a nucleic acid product, that product would end at about nucleotide 797, or about encoded amino acid 265 of the claimed CstI polypeptides. The amended claims are directed to CstI polypeptides comprising 1-328 or 1-430 amino acids of SEQ ID NO:2 and proteins with 95% identity to those sequences. Thus, the '756 patent primers (SEQ ID NO:46 and 47) cannot be used to produce a nucleic acid that would encode the claimed functional CstI polypeptides. The polypeptides claimed by the present application and the '756 patent are, therefore, patentably distinct and this rejection for alleged obviousness-type double patenting should be withdrawn.

Imtc
4/11/07
RF 1479M

PATENT

VI. Rejections under 35 U.S.C. §112, second paragraph

Claims 35-50 are rejected because the phrase "over the entire length" is allegedly indefinite. Applicants respectfully traverse the rejection and submit that, as amended, the claims are not indefinite. Moreover, the Office Action indicates that the rejections for alleged indefiniteness can be obviated by amending the claims to recite "wherein the α-2,3-sialyltransferase polypeptide comprises the amino acid sequence of residues 1-328 of SEQ ID NO:2 or an amino acid sequence that shares at least 95% identity with amino acid residues 1-328 of SEQ ID NO:2." *See, i.e.*, Office Action at page 7. In view of these amendments and remarks, withdrawal of the rejection for alleged indefiniteness is respectfully requested.

CONCLUSION

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance and an action to that end is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,

Beth E. Kelly
Reg. No. 51,868

TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center, Eighth Floor
San Francisco, California 94111-3834
Tel: 415-576-0200
Fax: 415-576-0300
Attachments
BLK:blk
60991916 v1

EMBOSS Align Results

Needle Results	
Matrix	Blosum62
Open gap penalty	10.0
Gap extension penalty	0.5
Needle output	needle-20070308-23144402448256.output

SUBMIT ANOTHER JOB

```
########################################
# Program:  needle
# Rundate:  Thu Mar 08 23:14:44 2007
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20070308-23144402448256.output
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: seq T from present app
# 2: rev 47 from '756 patent
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1293
# Identity:      28/1293 ( 2.2%)
# Similarity:    28/1293 ( 2.2%)
# Gaps:        1252/1293 (96.8%)
# Score: 110.0
#
#
#=======================================

seq                1 atgacaaggactagaatggaaaatgaactcattgttagtaaaaatatgca     50

rev                1                                                       0

seq               51 aaatataatcatagcaggaaatggacctagcctaaaaaatattaattata    100

rev                1                                                       0

seq              101 aaagactgcctagagaatatgatgtttttaggtgtaaccagttttatttt    150

rev                1                                                       0

seq              151 gaagataagtattatttaggaaaaaagattaaagcagtatttttttaatcc    200

rev                1                                                       0

seq              201 tggtgtctttttacaacagtatcacactgcaaaacaacttatactaaaaa    250

rev                1                                                       0

seq              251 atgagtatgaaataaaaaatatttttttgctctacatttaatttacctttt    300

rev                1                                                       0
```

EXHIBIT A

```
seq        301 attgaaagcaatgatttttacatcaattttataatttttccccgatgc  350
rev          1                                                    0
seq        351 aaaacttggctatgaagttattgaaaaccttaaagaattttatgcttata  400
rev          1                                                    0
seq        401 taaaatacaatgaaatttatttcaataaaagaattacttcgggcgtctat  450
rev          1                                                    0
seq        451 atgtgtgcaattgctattgcattaggatataaaaccatctatttatgtgg  500
rev          1                                                    0
seq        501 cattgatttttatgaaggagatgttatttatccttttgaagctatgagta  550
rev          1                                                    0
seq        551 caaatataaaaacaatctttcctggaataaaagatttcaaaccttcaaat  600
rev          1                                                    0
seq        601 tgtcattctaaggaatacgatatagaagcattaaaattgttaaaatcaat  650
rev          1                                                    0
seq        651 atacaaagttaatatctacgcattgtgtgatgattctattttggcaaatc  700
rev          1                                                    0
seq        701 attttcctttatcaattaatattaataacaatttcactttagaaaataag  750
                                                    ||.|..|||
rev          1                                     GATATAAAG      9
seq        751 cataataattctataaatgatattttattgactgataatactcctggcgt  800
                |||  ||.|||   |||.||.|.|...|.|||         |..||
rev         10 CAT--TATTTC---AAAGGAAAATAAGTCGAC----------CTAGG     41
seq        801 aagtttttataaaaatcaacttaaagctgataataaaattatgcttaatt  850
rev         42                                                   41
seq        851 tttataatattcttcattctaaagataatttaattaaatttttaaacaaa  900
rev         42                                                   41
seq        901 gaaattgcggtattaaaaaaacaaaccactcaacgagctaaagcaagaat  950
rev         42                                                   41
seq        951 ccaaaaccatctatcctataaactaggacaagctttgattataaattcta 1000
rev         42                                                   41
seq       1001 aaagtgtattaggtttttatctttaccttttataatattaagtatcgtt 1050
rev         42                                                   41
seq       1051 atttcacataaacaagaacaaaaggcttataaatttaaagtaaagaaaaa 1100
rev         42                                                   41
seq       1101 tccaaatttagctttacctcctttagaaacttatcctgattataatgaag 1150
```

```
rev              42                                                  41
seq            1151 ctttaaaagaaaaagaatgttttacttataaattaggagaagaatttata  1200
rev              42                                                  41
seq            1201 aaagctggtaagaattggtatggggaggggtatatcaaatttatattcaa  1250
rev              42                                                  41
seq            1251 agatgttcctaggttgaagagagagtttgagaaaggggaataa    1293
rev              42                                            41

#---------------------------------------
#---------------------------------------
```

EMBOSS Align Results

Needle Results	
Matrix	Blosum62
Open gap penalty	10.0
Gap extension penalty	0.5
Needle output	needle-20070308-23114566849720.output

SUBMIT ANOTHER JOB

```
########################################
# Program:  needle
# Rundate:  Thu Mar 08 23:11:46 2007
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20070308-23114566849720.output
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: seq 1 from present application
# 2: seq 46 from '756 patent
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1293
# Identity:      28/1293 ( 2.2%)
# Similarity:    28/1293 ( 2.2%)
# Gaps:        1252/1293 (96.8%)
# Score: 130.0
#
#
#=======================================

seq                1 atgacaaggactagaatggaaaatgaactcattgttagtaaaaaatatgca     50
                                                 |.|.|...||   .|||||.|
seq                1                                 CTTAGGAGGT---CATATGAA     18

seq               51 aaatataatcatagcaggaaatggacctagcctaaaaaatattaattata    100
                     |||..|.||.||.||.|||||||
seq               19 AAAAGTTATTATTGCTGGAAATG                               41

seq              101 aaagactgcctagagaatatgatgttttaggtgtaaccagttttatttt    150

seq               42                                                      41

seq              151 gaagataagtattatttaggaaaaaagattaaagcagtatttttaatcc    200

seq               42                                                      41

seq              201 tggtgtctttttacaacagtatcacactgcaaaacaacttatactaaaaa    250

seq               42                                                      41

seq              251 atgagtatgaaataaaaaatatttttgctctacatttaatttacctttt    300

seq               42                                                      41
```

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seq          301 attgaaagcaatgatttttacatcaattttataatttttccccgatgc  350
seq           42                                                   41
seq          351 aaaacttggctatgaagttattgaaaaccttaaagaattttatgcttata  400
seq           42                                                   41
seq          401 taaaatacaatgaaatttatttcaataaaagaattacttcgggcgtctat  450
seq           42                                                   41
seq          451 atgtgtgcaattgctattgcattaggatataaaaccatctatttatgtgg  500
seq           42                                                   41
seq          501 cattgatttttatgaaggagatgttatttatccttttgaagctatgagta  550
seq           42                                                   41
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seq           42                                                   41
seq          601 tgtcattctaaggaatacgatatagaagcattaaaattgttaaaatcaat  650
seq           42                                                   41
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seq           42                                                   41
seq          701 attttcctttatcaattaatattaataacaatttcactttagaaaataag  750
seq           42                                                   41
seq          751 cataataattctataaatgatattttattgactgataatactcctggcgt  800
seq           42                                                   41
seq          801 aagttttataaaaatcaacttaaagctgataataaaattatgcttaatt  850
seq           42                                                   41
seq          851 tttataatattcttcattctaaagataatttaattaaatttttaaacaaa  900
seq           42                                                   41
seq          901 gaaattgcggtattaaaaaaacaaaccactcaacgagctaaagcaagaat  950
seq           42                                                   41
seq          951 ccaaaaccatctatcctataaactaggacaagctttgattataaattcta 1000
seq           42                                                   41
seq         1001 aaagtgtattaggtttttatctttacctttttataatattaagtatcgtt 1050
seq           42                                                   41
seq         1051 atttcacataaacaagaacaaaaggcttataaatttaaagtaaagaaaaa 1100
seq           42                                                   41
seq         1101 tccaaatttagctttacctcctttagaaacttatcctgattataatgaag 1150
```

```
seq              42                                                  41
seq            1151 ctttaaaagaaaaagaatgttttacttataaattaggagaagaatttata 1200
seq              42                                                  41
seq            1201 aaagctggtaagaattggtatggggaggggtatatcaaatttatattcaa 1250
seq              42                                                  41
seq            1251 agatgttcctaggttgaagagagagtttgagaaaaggggaataa   1293
seq              42                                                41

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```